1600

RAW SEQUENCE LISTING   DATE: 01/27/2003
PATENT APPLICATION: **US/09/601,168B**   TIME: 10:53:49

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01242003\I601168B.raw**

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 3 <110> APPLICANT: BENAROUS, Richard·
 4        MARGOTTIN, Florence
 5        DURAND, Herve
 6        ARENZANA SEISDEDOS, Fernando
 7        KROLL, Mathias
 8        CONDORCET, Jean-Paul
10 <120> TITLE OF INVENTION: Human beta-TrCP protein
12 <130> FILE REFERENCE: 935.38812X00
14 <140> CURRENT APPLICATION NUMBER: US/09/601,168B
15 <141> CURRENT FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00196
18 <151> PRIOR FILING DATE: 1999-01-29
20 <150> PRIOR APPLICATION NUMBER: FR98 01100
21 <151> PRIOR FILING DATE: 1998-01-30
23 <150> PRIOR APPLICATION NUMBER: FR98 15545
24 <151> PRIOR FILING DATE: 1998-12-09
26 <160> NUMBER OF SEQ ID NOS: 9
28 <170> SOFTWARE: PatentIn Ver. 2.1 and manually
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2151
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial sequence
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (70)..(1776)
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA
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43 <400> SEQUENCE: 1
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46 tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111
47           Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
48            1               5                  10
50 ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct   159
51 Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro
52  15              20                  25                  30
54 agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc   207
55 Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser
56              35           .           40                  45
58 tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act   255
59 Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr
60              50                  55                  60
62 gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc   303
```

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 63 Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly
 64         65              70          75
 66 act tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat   351
 67 Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr
 68         80              85          90
 70 gaa aag gaa aag gaa ctg tgt gtc aaa tac ttt gag cag tgg tca gag   399
 71 Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu
 72 95              100         105             110
 75 tca gat caa gtg gaa ttt gtg gaa cat ctt ata tcc caa atg tgt cat   447
 76 Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His
 77             115             120             125
 79 tac caa cat ggg cac ata aac tcg tat ctt aaa cct atg ttg cag aga   495
 80 Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg
 81             130             135             140
 83 gat ttc ata act gct ctg cca gct cgg gga ttg gat cat atc gct gag   543
 84 Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu
 85         145             150             155
 87 aac att ctg tca tac ctg gat gcc aaa tca cta tgt gct gct gaa ctt   591
 88 Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu
 89         160             165             170
 91 gtg tgc aag gaa tgg tac cga gtg acc tct gat ggc atg ctg tgg aag   639
 92 Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys
 93 175             180             185             190
 95 aag ctt atc gag aga atg gtc agg aca gat tct ctg tgg aga ggc ctg   687
 96 Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu
 97             195             200             205
 99 gca gaa cga aga gga tgg gga cag tat tta ttc aaa aac aaa cct cct   735
100 Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro
101             210             215             220
103 gac ggg aat gct cct ccc aac tct ttt tat aga gca ctt tat cct aaa   783
104 Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys
105         225             230             235
107 att ata caa gac att gag aca ata gaa tct aat tgg aga tgt gga aga   831
108 Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg
109         240             245             250
111 cat agt tta cag aga att cac tgc cga agt gaa aca agc aaa gga gtt   879
112 His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val
113 255             260             265             270
115 tac tgt tta cag tat gat gat cag aaa ata gta agc ggc ctt cga gac   927
116 Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp
117             275             280             285
119 aac aca atc aag atc tgg gat aaa aac aca ttg gaa tgc aag cga att   975
120 Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile
121             290             295             300
123 ctc aca ggc cat aca ggt tca gtc ctc tgt ctc cag tat gat gag aga  1023
124 Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg
125         305             310             315
127 gtg atc ata aca gga tca tcg gat tcc acg gtc aga gtg tgg gat gta  1071
128 Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val
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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/601,168B**

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129      320                       325                    330
131 aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt  1119
132 Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val
133 335                       340                    345                    350
136 ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat  1167
137 Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp
138                       355                    360                    365
140 cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc  1215
141 Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu
142                   370                    375                    380
144 cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt  1263
145 Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe
146               385                    390                    395
148 gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta  1311
149 Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val
150       400                    405                    410
152 tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa  1359
153 Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys
154 415                    420                    425                    430
156 cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc  1407
157 Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly
158                   435                    440                    445
160 tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt  1455
161 Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys
162               450                    455                    460
164 tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt  1503
165 Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe
166           465                    470                    475
168 gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg  1551
169 Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val
170       480                    485                    490
172 tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc  1599
173 Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu
174 495                    500                    505                    510
176 tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag  1647
177 Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln
178               515                    520                    525
180 ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc  1695
181 Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu
182               530                    535                    540
184 atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt  1743
185 Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg
186           545                    550                    555
188 tcc cct tct cga aca tac acc tac atc tcc aga taaataacca tacactgacc  1796
189 Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
190       560                    565
192 tcatacttgc ccaggaccca ttaaagttgc ggtatttaac gtatctgcca ataccaggat  1856
194 gagcaacaac agtaacaatc aaactactgc ccagtttccc tggactagcc gaggagcagg  1916
196 gctttgagac tcctgttggg acacagttgg tctgcagtcg gcccaggacg gtctactcag  1976
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198 cacaactgac tgcttcagtg ctgctatcag aagatgtctt ctatcaattg tgaatgattg 2036
200 gaacttttaa acctcccctc ctctcctcct ttcacctctg cacctagttt tttcccattg 2096
202 gttccagaca aaggtgactt ataaatatat ttagtgtttt gccagaaaaa aaaaa       2151
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 569
206 <212> TYPE: PRT
207 <213> ORGANISM: Artificial sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA
211        coding for human beta-TrCP protein
214 <400> SEQUENCE: 2
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216  1               5                  10                  15
218 Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
219             20                  25                  30
221 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
222         35                  40                  45
224 Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
225     50                  55                  60
227 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
228 65                  70                  75                  80
230 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
231             85                  90                  95
233 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
234             100                 105                 110
236 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
237             115                 120                 125
239 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
240     130                 135                 140
242 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
243 145                 150                 155                 160
245 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
246             165                 170                 175
248 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
249             180                 185                 190
251 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
252     195                 200                 205
254 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
255     210                 215                 220
257 Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
258 225                 230                 235                 240
260 Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
261             245                 250                 255
263 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
264             260                 265                 270
268 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
269         275                 280                 285
271 Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
272     290                 295                 300
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/601,168B

DATE: 01/27/2003
TIME: 10:53:50

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01242003\I601168B.raw**

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274 Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
275 305                 310             315             320
277 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
278                 325             330             335
280 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
281             340             345             350
283 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
284         355             360             365
286 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
287     370             375             380
289 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
290 385                 390             395             400
292 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
293             405             410             415
295 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
296         420             425             430
298 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
299     435             440             445
301 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
302     450             455             460
304 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
305 465                 470             475             480
307 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
308             485             490             495
310 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
311             500             505             510
313 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
314         515             520             525
316 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
317     530             535             540
319 Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro
320 545             550             555             560
322 Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
323             565
326 <210> SEQ ID NO: 3
327 <211> LENGTH: 19
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of the artificial sequence : sense primer
334 <400> SEQUENCE: 3
335 ccaaactgcg tataacgcg                                              19
338 <210> SEQ ID NO: 4
339 <211> LENGTH: 20
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Description of the artificial sequence : antisense primer
346 <400> SEQUENCE: 4
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: **US/09/601,168B**

DATE: 01/27/2003
TIME: 10:53:51

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\01242003\I601168B.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 4,5